Table S1. Current literature data about proper mtDNA level evaluation in blood sample

Study reference	Methodical issue	Relevant findings
Kalinowski et al., 1992	Determination of the influence of lesion frequencies on mtDNA level estimation	Increasing error in mtDNA amount evaluation is correlated with higher template fragmentation level
Bremen et al., 1999	Comparison the most common elements of DNA extraction and purification protocols	Using phenol method to DNA extraction can inhibit PCR reaction due to the presence of e.g. residues of ethanol, proteins or divalent cations
Chen et al., 2007	Appropriate period of time to conduct DNA isolation	Isolation of DNA within 4 hours after blood collection
Adreu et al., 2009	Evaluation of several factors, materials and DNA extraction method, which can affect measurement of mtDNA content	Isolation from whole blood brings higher mtDNA level than buffy coat samples. DNA extraction method may have impact on mtDNA level quantification. The column technique showed the greatest precision and repeatability
Malik et al., 2011	Description of PCR-based method using unique regions in the human mitochondrial genome not duplicated in the nuclear genome	Possibility of duplicated mitochondrial genome into the nuclear genome and present of pseudogenes in nDNA must be considerate during primer design
Côté et al., 2011	Impact of type of results analyses on mtDNA level in different laboratories	There is wide variation when absolute analysis was conducted, however using relative values leads to some consensus between result

References:

Andreu, A. L., Martinez, R., Marti, R., & García-Arumí, E. (2009). Quantification of mitochondrial DNA copy number: Pre-analytical factors. *Mitochondrion*, *9*(4), 242–246. https://doi.org/10.1016/j.mito.2009.02.006

Bremen, S. U., Miller, D. N., Bryant, J. E., Madsen, E. L., & Ghiorse, W. C. (1999). Evaluation and Optimization of DNA Extraction and Purification Procedures for Soil and Sediment Samples Evaluation and Optimization of DNA Extraction and Purification Procedures for Soil and Sediment Samples, *65*(11), 4715–4724.

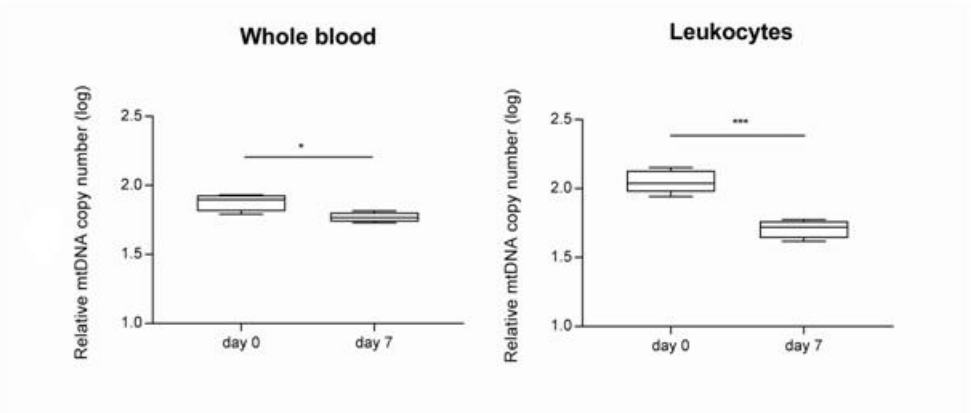
Chen, C. M., Wu, Y. R., Cheng, M. L., Liu, J. L., Lee, Y. M., Lee, P. W., … Chiu, D. T. Y. (2007). Increased oxidative damage and mitochondrial abnormalities in the peripheral blood of Huntington's disease patients. *Biochemical and Biophysical Research Communications*, *359*(2), 335–340. https://doi.org/10.1016/j.bbrc.2007.05.093

Côté, H. C. F., Gerschenson, M., Walker, U. A., Miro, O., Garrabou, G., Hammond, E., … Cossarizza, A. (2011). Quality assessment of human mitochondrial DNA quantification: MITONAUTS, an international multicentre survey. *Mitochondrion*, *11*(3), 520–7. https://doi.org/10.1016/j.mito.2011.01.011

Kalinowski, D. P., Illenye, S., & Van Houten, B. (1992). Analysis of DNA damage and repair in murine leukemia L1210 cells using a quantitative polymerase chain reaction assay. *Nucleic Acids Research*, *20*(13), 3485–94. Retrieved from http://www.ncbi.nlm.nih.gov/pubmed/1630919

Malik, A. N., Shahni, R., Rodriguez-de-Ledesma, A., Laftah, A., & Cunningham, P. (2011). Mitochondrial DNA as a non-invasive biomarker: Accurate quantification using real time quantitative PCR without co-amplification of pseudogenes and dilution bias. *Biochemical and Biophysical Research Communications*, *412*(1), 1–7. https://doi.org/10.1016/j.bbrc.2011.06.067

Figure S1. Levels of mtDNA is blood samples of the same patients withdrawn during 7 day interval. Samples were stored for 3 days at - 20ºC. The "repeated measures" t-test on log-transformed data: *$p < 0.05$, ** $p < 0.01$, ***$p < 0.001$.


Whole blood
Relative mtDNA copy number (log)
2.5
2.0
1.5
1.0
*
day 0
day 7
Leukocytes
Relative mtDNA copy number (log)
2.5
2.0
1.5
1.0
***
day 0
day 7